

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2003, 06:34:51 ; Search time 46 Seconds
(without alignments)
1688.690 Million cell updates/sec

Title: US-10-091-628-2
Perfect score: 1979
Sequence: 1 MRANSSSSACPPANSSEEL.....FGPMCHRALPVGHTSC 377.

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL 21.*

- 1: sp archaea:*
- 2: sp bacteria:*
- 3: sp fungi:*
- 4: sp human:*
- 5: sp invertebrate:*
- 6: sp mammal:*
- 7: sp mhc:*
- 8: sp organelle:*
- 9: sp phage:*
- 10: sp plant:*
- 11: sp rodent:*
- 12: sp virus:*
- 13: sp vertebrate:*
- 14: sp unclassified:*
- 15: sp virus:*
- 16: sp bacteriophage:*
- 17: sp archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1415	71.5	373	11 Q9CXB2	Q9CXB2 mus musculu
2	871	44.0	348	11 P70172	P70172 mus musculu
3	866	43.8	348	11 Q925U7	Q925U7 mus musculu
4	567.5	26.7	348	6 Q97736	Q97736 oryctolagus
5	546	27.6	317	11 Q35940	Q35940 mus musculu
6	535	27.0	437	4 Q8WU22	Q8WU22 homo sapien
7	535	27.0	462	4 Q96EP9	Q96EP9 homo sapien
8	352	17.8	125	11 Q8V183	Q8V183 mus musculu
9	351.5	17.7	187	11 Q8QZJ2	Q8QZJ2 mus musculu
10	351	16.9	448	4 Q9BSI2	Q9BSI2 mesocricetu
11	333.5	16.9	321	16 Q34524	Q34524 bacillus su
12	325	16.4	305	16 Q99RV2	Q99RV2 staphylococ
13	301.5	15.2	318	16 Q9Y106	Q9Y106 bruceella me
14	299.5	15.1	323	16 Q9KEJ4	Q9KEJ4 bacillus ha
15	284	14.4	338	10 Q81017	Q81017 arabidopsis

17	277	14.0	408	10 Q9AS49	Q9AS49 oryza sativ
18	276	13.9	409	10 Q8S2V7	Q8S2V7 arabidopsis
19	269.5	13.6	311	16 Q9HYX6	Q9HYX6 pseudomonas
20	266.5	13.5	315	16 Q9K0A9	Q9K0A9 neisseria m
21	266.5	13.5	338	17 Q8TPB0	Q8TPB0 methanosaer
22	266	13.4	455	5 Q9VXV4	Q9VXV4 drosophila
23	265.5	13.4	315	16 Q9JVB5	Q9JVB5 neisseria m
24	257.5	13.0	297	16 Q9J375	Q9J375 pseudomonas
25	250	12.6	297	16 Q67889	Q67889 aquifex aeo
26	240	12.1	401	10 Q93YR2	Q93YR2 arabidopsis
27	239	12.1	454	5 Q9VXF5	Q9VXF5 drosophila
28	238.5	12.1	292	16 P73338	P73338 synechocyst
29	230	11.6	325	16 Q9KZG2	Q9KZG2 streptomyce
30	228.5	11.5	313	16 Q8XK10	Q8XK10 salmoneilla
31	223	11.3	207	16 Q8U766	Q8U766 agrobacteri
32	222.5	11.2	318	16 Q9JX64	Q9JX64 neisseria m
33	219.5	11.1	298	16 Q8YLP2	Q8YLP2 anabaena sp
34	211	10.7	409	10 Q8VYX4	Q8VYX4 mus musculu
35	173	8.7	409	10 Q8VYX4	Q8VYX4 arabidopsis
36	171	8.6	460	10 Q49665	Q49665 arabidopsis
37	170	8.6	273	10 Q94A17	Q94A17 arabidopsis
38	156	7.9	379	10 Q9S268	Q9S268 arabidopsis
39	150	7.6	431	10 Q8RXE8	Q8RXE8 arabidopsis
40	142	7.6	454	10 Q9LSV9	Q9LSV9 arabidopsis
41	140	7.2	344	16 Q86662	Q86662 streptomyce
42	132	6.7	288	17 Q8TWM4	Q8TWM4 methanosaer
43	124	6.3	303	8 Q8SEV7	Q8SEV7 leptura arc
44	121.5	6.1	324	16 Q9X005	Q9X005 thermotoga
45	121	6.1	612	3 Q74395	Q74395 schizosacch

ALIGNMENTS

RESULT 1	ID	Q9CXB2	PRELIMINARY:	PRT:	373 AA.
AC	Q9CXB2	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE	8430417G17RIK protein.				
GN	8430417G17RIK.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batlov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Glisic C., King B., Koehwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki K., Tomita M., Wagner L., Washio T.,				
RA	Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzaletti U., Mombereis P.,				
RA	Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,				
RA	Hayashizaki Y.,				
RT	"Functional annotation of a full-length mouse cDNA collection."				
RL	Nature 409:685-690(2001).				
DR	EMBL; AK018423; BAB31203.1; -				
DR	MGD; MGI:1923000; 8430417G17RIK.				

Db 183 NHKWPQAKIILKIGSITGVILVILAVIGLILYOSAWIIEPKMLIGTIPPIAGSYSGF 242
 QY 243 LIALFTHOSMORCRITISLETGAONIOMCTIMLQSFTHAHLVOMLSFPLAYGLFOLLIDGF 302
 Db 243 FLARLAGQWYKCRVIALETGOMQTOLCSTIVQLSFPEDLIVTFPLPIYVFOQVPA 302
 QY 303 LIVAAYQYVYKRLKKNHKGKNSGCTEVCHTRKSTSR---ETNAFLEVNEE 350
 Db 303 VILGIYVYTRK---CYGNDAEPLE--RTDNEMSRSPFDETNNGFQDDEK 348

RESULT 4

097736 PRELIMINARY; PRT; 348 AA.

AC 097736
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 Hepatic sodium-dependent bile acid transporter.
 Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stengel S, Becker W, Maier M, Noll R, Kramer W;
 RT "Rabbit cDNA encoding hepatic sodium-dependent bile acid
 transporter.";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ131361; CA10360.1; -
 DR InterPro: IPR004710; Bases.
 DR InterPro: IPR002657; BileAc/Na_smprtr.
 DR Pfam: PF01758; SBF; 1.
 DR TIGRfams: TIGR00841; Bases; 1.
 DR TIGRfams: TIGR00841; Bases; 1.
 SQ SEQUENCE 348 AA; 37932 MW; 992A08F4AAA4489B CRC64;

Query Match 28.7%; Score 567.5; DB 6; Length 348;
 Best Local Similarity 38.9%; Pred. No. 8.5e-39;
 Matches 112; Conservative 69; Mismatches 100; Indels 7; Gaps 3;

QY 31 ELVFTVSTVMGMLMFLSGSVEIRKLSHRRPWGIAVGLLCOFGIMPTAYLLAISF 90
 Db 24 DLALSVILVIMLTIMLSIGCTMEFSKIKAHFLKPGALIALVAQYIMPLTAFLVGLKF 83
 QY 91 SLKPVQALVILMGCCPGGTISNIFFWVDGMDLSMTTGSTVALGMPPLCIYLT- 149
 Db 84 RNMNIEALAILVCGSPGNSMFLSLAVKGDMLISVMTTSTFLALGMPPLLIYISR 143
 QY 150 --MSWSLQONLITPYONIGITVCLTIPVAFGVYVYRMPKOSKILKIGAVVGVLLV 207
 Db 144 GYEBDLKQK--VPYIGMISLMIIPCTIGIILSKRPQYVYIKVGIITTSISIA 201
 QY 208 VAVAGVVLAKGSNMSDIT--LLTISPIPLIGHVTPLLALFTHOSMORCRITISLETGAO 265
 Db 202 VAVLAINVNGNSIMVMTYPLTISALMPFIFGLFISALFRLSARCSRTISMETGQ 261
 QY 266 NIGMCTIMQLSTFAHLVOMLSFPLAYGLFOLLIDFLLVAAYQYTKR 313
 Db 262 NVQLSTILNVTFAPEVIGLFFPFLYIMFOLAEGLIIAIVRCYEC 309

RESULT 5

035940 PRELIMINARY; PRT; 317 AA.

AC 035940
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Na/taurocholate cotransporting polypeptide 2.
 GN SLC10A1 OR NTCF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BAB/C;
 RA Hagenbuch B.;
 RT "Identification of two forms of the Na/taurocholate cotransporting
 RT polypeptide in mouse liver.";
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U95132; AAB81024.1; -
 DR MGI; MGI:97379; SLC10A1.
 DR InterPro: IPR004710; Bases.
 DR InterPro: IPR002657; BileAc/Na_smprtr.
 DR Pfam; PF01758; SBF; 1.
 DR TIGRfams: TIGR00841; Bases; 1.
 SQ SEQUENCE 317 AA; 3486 MW; DA32C829C8ABE6D0 CRC64;

Query Match 27.6%; Score 546; DB 11; Length 317;
 Best Local Similarity 37.2%; Pred. No. 4.5e-37;
 Matches 118; Conservative 70; Mismatches 117; Indels 12; Gaps 6;

QY 10 ACPANSSSEELPVGLEVGNLEIVFTVSTVMGMLMFLSGSVEIRKLSHRRPWGIA 69
 Db 7 SAPFNFS--LPFGG-HRAVDTLSTLVVMLLIMLSLCTMEFSKIKAHFWKPKVIT 62
 QY 70 VGLLCOFGIMPTAYLLAISFSLKPVQALVILMGCCPGGTISNIFFWVDGMDLSISM 129
 Db 63 IAIYVQYIMPLSAFLKGVHLHSIEALILICGCSGNSLFTLAMGDMNLISVM 122
 QY 130 TTCSTVALGMPPLCIYLT--MSWSLQONLITPYONIGITVCLTIPVAFGVYVYRW 186
 Db 123 TTCSSFTALGMPPLLIYISKGIYDGLKDK--VPYKGMISLWVLLIPCAIGIFLKSQR 180
 QY 167 PKOSKILKIGAVVGVLLVAVAGVVLAKGSNMSDIT--LLTISPIPLIGHVTPGL 244
 Db 161 PHVYVYKAGKITIFSLSVAVTVLSTVNGNSIMFWTPHLATSSLMPTGLMGIYL 240
 QY 245 ALFTHOSMORCRITISLETGAONIOMCTIMLQSFTHAHLVOMLSFPLAYGLFOLLIDGFLI 304
 Db 241 SALFPLNMSCRTISMETGQNVQLSTILNVTFAPEVIGLFFPFLYIMFOLAEGLIF 300
 QY 305 VAAVQYKRLKKNHKGK 321
 Db 301 IIFRCY-LKIKPKQK 316

RESULT 6

08WU22 PRELIMINARY; PRT; 437 AA.

ID 08WU22
 AC 08WU22
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DE Hypothetical 46.5 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC019066; AAH19066.1; -
 DR InterPro: IPR002657; BileAc/Na_smprtr.
 DR Pfam; PF01758; SBF; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 437 AA; 46503 MW; 055E989629CC13D1 CRC64;

Query Match 27.0%; Score 535; DB 4; Length 437;
 Best Local Similarity 35.7%; Pred. No. 5e-36;
 Matches 111; Conservative 59; Mismatches 101; Indels 40; Gaps 5;

QY 27 HGNLVLFTVSTVMGMLMFLSGSVEIRKLSHRRPWGIAVGLLCOFGIMPTAYLL 86

```

Db      103 HGNLNFVGAALCTTMMG-----IGCTVDVNHFGAHRPRPGALLAALCOFGLPLLAFL 157
QY      87 AIFSFLKPVQALAVLIMGCCPGGTINIFFWGDMDSISMTTCTVAALGMPFLCY 146
Db      158 ALAFKIDEVAAVAVLCCGCGGNTLSNLSLVDGDMNISITITSTLALVLMPLCLM 217
QY      147 LYTWSN---SLOONLTIPTVONIGITLVCLTIPTVAFGVYVYVYRMPKSKIIILKI----- 196
Db      218 IYSWAMINPIVQ--LLPLGTVTLTLCSTLIPGLGVFIRKYSRVADYIVKVSLSMLLV 275
QY      197 -----GAVVGVLLVVAAGVVLAKGSWNSDITLTITSFIRPLIGHVTFGLALF 247
Db      276 TLVVLFIPTGTMTGPELLASIPAAVYIA-----IFMPLAGVAGSYGLATL 321
QY      248 THOSMORCRTISLETGAQNIOMCTIMOLSFTEHVLQMSLFPPLAYGLFQILDGFLIIVA 307
Db      322 FLHPKCKRTVCLETGSQNVQCTALIKLAFPPQFISGMYMFLYALFQSAEAGIFVLI 381
QY      308 YQTYKRLKXK 318
        382 YKMGSEMLHK 392

```

RESULT 7

```

Q96EP9 ID Q96EP9 PRELIMINARY; PRT; 462 AA.
AC Q96EP9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unknown (Protein for IMAGE:3502817) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Strausberg R.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012048; AAH12048.1; -
DR InterPro; IPR002657; BileAc/Na_smptr.
DR Pfam; PF01758; SBF; 1.
FT NON_TER
SQ SEQUENCE 462 AA; 49035 MW; B916D68AE40622C CRC64;

```

Query Match 27.0%; Score 535; DB 4; Length 462;

Best Local Similarity 35.7%; Pred. No. 5.3e-36; Mismatches 101; Indels 40; Gaps 5;

```

Matches 11; Conservative 59; Mismatches 101; Indels 40; Gaps 5;
QY      27 HGNLIEVFTVSTVMGMLMFSLGSEVIRKLSHRRPWGIVAGLCOFGLMPTAYLL 86
Db      128 HGNLNFVGAALCTTMMG-----IGCTVDVNHFGAHRPRPGALLAALCOFGLPLLAFL 182
QY      87 AIFSFLKPVQALAVLIMGCCPGGTINIFFWGDMDSISMTTCTVAALGMPFLCY 146
Db      183 ALAFKIDEVAAVAVLCCGCGGNTLSNLSLVDGDMNISITITSTLALVLMPLCLM 242
QY      147 LYTWSN---SLOONLTIPTVONIGITLVCLTIPTVAFGVYVYVYRMPKSKIIILKI----- 196
Db      243 IYSWAMINPIVQ--LLPLGTVTLTLCSTLIPGLGVFIRKYSRVADYIVKVSLSMLLV 300
QY      197 -----GAVVGVLLVVAAGVVLAKGSWNSDITLTITSFIRPLIGHVTFGLALF 247
Db      301 TLVVLFIPTGTMTGPELLASIPAAVYIA-----IFMPLAGVAGSYGLATL 346
QY      248 THOSMORCRTISLETGAQNIOMCTIMOLSFTEHVLQMSLFPPLAYGLFQILDGFLIIVA 307
Db      347 FLHPKCKRTVCLETGSQNVQCTALIKLAFPPQFISGMYMFLYALFQSAEAGIFVLI 406
QY      308 YQTYKRLKXK 318
        382 YKMGSEMLHK 392

```

Db 407 YKMGSEMLHK 417

RESULT 8

```

Q8V183 ID Q8V183 PRELIMINARY; PRT; 125 AA.
AC Q8V183;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Ilean sodium-dependent bile acid transporter (Fragment).
GN ISBT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Saeki T., Kirifuji K., Kanamoto R., Iwami K.;
RT "Identification of transcription start sites in mouse ileal sodium-
RT dependent bile acid transporter gene."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078635; BAB84081.1; -
DR InterPro; IPR002657; BileAc/Na_smptr.
DR Pfam; PF01758; SBF; 1.
FT NON_TER
SQ SEQUENCE 125 AA; 13275 MW; C7F8EFC459D4C8F7 CRC64;

```

Query Match 17.8%; Score 352; DB 11; Length 125;

Best Local Similarity 52.0%; Pred. No. 1.5e-21; Mismatches 64; Conservative 25; Mismatches 30; Indels 4; Gaps 2;

```

QY      7 SSSACPANSS--EEELPYGLEVHGN--LELVTVVSTVMGMLMFSLGSEVIRKLSH 62
Db      3 NSVCPNATVCEGDSQVPEENFNAINTVWSTVLITLAMVMSGCVNVEVHFLGHI 62
QY      63 RRPWGIVAGLCOFGLMPTAYLLAIFSFLKPVQALAVLIMGCCPGGTINIFFWGDM 122
Db      63 KRPWGIFFVGLCOFGLMPTAYLLAIFSFLKPVQALAVLIMGCCPGGTINILAYWID 122
QY      123 MDL 125
Db      123 MDL 125

```

RESULT 9

Q8QZR2 ID Q8QZR2 PRELIMINARY; PRT; 473 AA.

```

AC Q8QZR2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein p3 (Hypotheetical 50.3 kDa protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBL_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC027440; AAH27440.1; -
DR EMBL; BC027440; AAH27440.1; -
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 50254 MW; 9A2ADDA005DD1805 CRC64;

```

Query Match 17.8%; Score 351.5; DB 11; Length 473;

Best Local Similarity 32.4%; Pred. No. 6.4e-21; Mismatches 91; Conservative 57; Mismatches 108; Indels 25; Gaps 5;

QY 11 CPANSEELPYGLEVH-GNLE--LVFTVSTVMGMLFSGSVIRKLSHRRPM 66
 DB 163 CIRVPAPBEPBALNINLGHFSENPILYLPLIFPNKSF--GCKVELEVKELIQSQ 220
 QY 67 GIAGVLLCGFGLMPFAYLLAISFSKPVQAVLIMGCCPGGTISNIFTFWVDGMDLS 126
 DB 221 PMLGLGLGFLVMPFAFLMAKVFMLPKALALGLITCS PGGGGSYLFSLGGLVTLA 280
 QY 127 ISMTGCTVPAALGMPICLYTWSLQONLTIPQONIGITVLCITIVAGVYVNRW 186
 DB 281 ISMTFISTVAAAGFLPLSSAIVSYLLSIHETLHPISKILGTLFLAIPAGAVIKSKL 340
 QY 187 PKOSKIILKIGAVGVLL-----VVAAGVVLAKGSWNSDITLITISFIFPLI 236
 DB 341 PFSESLLOVIRPFSESLILGLFLAYHMGVFLVGR-----PIVLGVFTVPLV 391
 237 GHVTFLLALFTHQSWQRCRTISLETGAONIQMTLMQLS 277
 392 GLVGVSLALCLKLPVAGQRTVSIKGVQNSLLALMLQLS 432

RESULT 10

Q9QZJ2 PRELIMINARY; PRT; 187 AA.

AC Q9QZJ2; PRELIMINARY; PRT; 187 AA.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAY-2002 (TREMblrel. 20, Last annotation update)
 DE Na-Taucocholate cotransporting polypeptide (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Balasubramanian N., Arrese M., Suchy F.J., Ananthanarayanan M.;
 RT "Na-Taucocholate cotransporting polypeptide (Ntcp) from Hamster
 RT liver".
 RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF181258; AAD53961.1;
 DR InterPro; IPR002657; BileAc/Na_smptr.
 DR Pfam; PF01758; SBF; 1.
 FT NON_TER 1, 187
 NON_TER 187
 SEQUENCE 187 AA; 20182 MW; 2855CSF44AB482C6 CRC64;

Query Match 17.7%; Score 351; DB 11; Length 187;
 Best Local Similarity 42.6%; Pred. No. 2.8e-21;
 Matches 80; Conservative 34; Mismatches 64; Indels 10; Gaps 5;

QY 75 QGIMPFAYLLAISFSKPVQAVLIMGCCPGGTISNIFTFWVDGMDLSISMTGCT 134
 DB 1 QGIMPLAFVNLKVFHLPBALAILICGSPGGLSNLFLAMGDVNLISVMTGCT 60
 QY 135 VALGMMPLICLYT---MSWSLQONLTIPQONIGITVLCITIVAGVYVNRWPKSK 191
 DB 61 FALGMMPLILYIKGIYDGLKOK--VPYGGIMISLVWVILPCLGIFLTKRQYVP 118
 QY 192 ILIKIGAVGVLLVAVAGVVLAKGSWNSDIT--LTITISFIFPLIGHVTFLL-ALPT 248
 DB 119 YIKGGMITFLISAVVYLSIINNGNSIKPAMTPPLATSSLPSSGFLGLYALSALF- 177
 QY 249 HQSQQR 256
 DB 178 -QLNPRCR 184

RESULT 11
 Q9BSL2 PRELIMINARY; PRT; 448 AA.
 AC Q9BSL2;

DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to protein p3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC004966; AA004966.1;
 DR InterPro; IPR004710; Baas.
 DR InterPro; IPR002657; BileAc/Na_smptr.
 DR Pfam; PF01758; SBF; 1.
 DR TIGRPFAMs; TIGR00841; baas; 1.
 SQ SEQUENCE 448 AA; 47548 MW; 47A1263CF8EFPF91 CRC64;

Query Match 16.9%; Score 333.5; DB 4; Length 448;
 Best Local Similarity 31.5%; Pred. No. 1.8e-19;
 Matches 87; Conservative 53; Mismatches 115; Indels 21; Gaps 3;

QY 12 PANSEELPYGLEVHGNLELVFTVSTVMGMLFSGSVIRKLSHRRPMGIWVG 71
 DB 143 PAEDPPLSLADLAFSENPILYLPLIFPNKSF--GCKVELEVKELIQSQPMLIG 200
 QY 72 ILICGIMPFAYLLAISFSKPVQAVLIMGCCPGGTISNIFTFWVDGMDLSISMT 131
 DB 201 ILICGIMPLVLAFLMAKVFMLPKALALGLITCS PGGGGSYLFSLGGLVTLAISM 260
 QY 132 CSTVALGMPICLYTWSLQONLTIPQONIGITVLCITIVAGVYVNRWPKSK 191
 DB 261 LSTVATGFLPLSSAIVSYLLSIHETLHPISKILGTLFLAIPAGVILKSKPKFSQ 320
 QY 192 ILIKIGAVGVLL-----VVAAGVVLAKGSWNSDITLITISFIFPLIGHV 241
 DB 321 LLQVVKRPFSPVLLGLGFLAYRMGVFLAGRL-----PIVLGITVPLVGLVG 371

QY 242 FLALFTHQSWQRCRTISLETGAONIQMTLMQLS 277
 DB 372 YCLATCLKLPVAGQRTVSIKGVQNSLLALMLQLS 407

RESULT 12

Q34524 PRELIMINARY; PRT; 321 AA.

AC Q34524;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Putative transporter.
 GN YOCs.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Baetoro M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghit S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haehe J., Harwood C.R., Henaut A.,
RA Hilbert H., Holtsappel S., Hosono S., Hultio M.F., Iraya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaeter-Blanchard M., Klein C.,
RA Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarovic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Prieecan E., Fujic P., Purnelle B., Kapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeder R., Scofield F.,
RA Sekiguchi Y., Sekowska A., Serró S.J., Serró P., Shin B.S., Soldo B.,
RA Sorokin A., Taccoti E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Tempesra P., Tognoni A.,
RA Toesato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Varti A., Wandut B., Wedler E., Wedler H., Weltzenegger T.,
RA Winters P., Wipal A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
"The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*,"
PL Nature 390:249-256 (1997).
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN=168;
RC
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/genbank/DBJ databases.
RR EMBL: AF027866; AAB84443.1; -
DR EMBL: Z99114; CAB13827.1; -
DR InterPro: IPR004710; Baas.
DR InterPro: IPR002657; BileAc/Na_smptr.
DR Pfam: PF01758; SBF; 1.
DR TIGRFAMs: TIGR00841; baas; 1.
KW Complete proteome.
SQ SEQUENCE 321 AA; 34251 MW; 0D9CCF6B3E84A96 CRC64;

Query Match 16.4%; Score 325; DB 16; Length 321;
Best Local Similarity 27.6%; Pred. No. 6.5e-19;
Matches 84; Conservative 76; Mismatches 114; Indels 30; Gaps 12;

33 VFTVVS---TVMGGLMPSLGSVEIRKLMSHRRPWSGAVGLLQFGGLMPTAVYLAIS 89
DB 32 LFTWISSITITFLGIITFGMGILTLQADDFKELVKKRPQVYIIVIAQITIMPLVAFGLAF 91
QY 90 FSLKRVQAIIVLIMGCGCGEGTISNIFTEWDDMDLSISMTCTSTVAALGMPLCIYLYT 149
DB 92 LHLPLRAIVAGVILVAGCCCGGTFASNWTFELAKGNLTALSAVVTITSTLLPAVTVPLLIIMFLA 151
150 WMSLSIQQLTIPYQNIIGITIV-CLTIPVAFGYVNVYRMPKO-SKII--LTKIGAVVGSVL 205
DB 152 KEW-----LPSPGSLFTSILDVAFLPITAGIIVMPFRKQVAKVHALPLVSVIG--- 202
QY 206 LVVAAGVAVLAKGSWN---SDITLLTISIFIFELGIIVGVFLTALFTHSWQRCRTISLET 262
DB 203 -IVAIIVSAVVSNGNRNLTQSGILIRISVILNHNGIGYLLGFLCAKLLKMDYSQKAIAREV 261
QY 263 GAONIQWCTIMTQLSFTAEHLVQMLSFPLA-YGLFQOLIDGFLIYVAAYOTYKRLKNKA-G 320
DB 262 GMON-----SGIGALATATAPSPISAVPSAIFSVMHNLGSGWL-ATY--WSKVKKKQAG 313
QY 321 KENS 324
DB 314 SKSS 317

RESULT 13
ID 099RV2 PRELIMINARY; PRT; 305 AA.
AC 099RV2.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DR	Hypothetical protein SAV2321.
GN	SAV2321 OR SA2112.
OS	Staphylococcus aureus (strain Mu50 / ATCC 700659), and
OC	Staphylococcus aureus (strain N315).
CC	Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OX	Staphylococcus.
RN	NCBI_TaxID=158879;
RP	[1]
RT	SEQUENCE FROM N.A.
RA	SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RL	MEDLINE=21311952; PubMed=11418146;
DR	EMBL, AP0031365; BAB58483.1; -
DR	EMBL, AP0031365; BAB58483.1; -
DR	InterPro, IPR02657; Billec/Ne_smprtc.
DR	Pfam, PF01758; SBF, 1.
KW	Hypothetical protein; Complete proteome.
SQ	SEQUENCE 305 AA; 32865 MW; 18423015196B657 CRC64;
Query Match	15.2%; Score 301.5; DB 16; Length 305;
Best Local Similarity	27.9%; Pred. NO. 5.3e-17;
Matches	68; Conservative 60; Mismatches 101; Indels 15; Gaps 4
QY	41 MGGILMFSLGSGVIRKLMHSIRRPWGIAGVLCOFGIMPTAYDLAISFSIKPVOAIAV 100
DB	41 LAGIVLMGMLTIRPNDEPKWFKAPRAVITIGVCLQFSIMPTLAFLIAKSFHLPDIAVGV 100
QY	101 LIMGCCRGRTISNFTFEWDDMDLSIMTTCSTYALAGMMPPLCYLYTWSLSQONLTI 160
DB	101 ILVCCPCPGTSSNWSYLAKANVALSVITTVSTLLAFVTPALTYLPRANEMLEVSFLSM 160
QY	161 PYQNIIGITLVCLTIPVAFGV--VYVYWPKOSKIILKIGAVGGLLVAVAG---VV 214
DB	161 LMSVVOYVL----IPALGIVLQIINRKIAKASALPLISIVMSLLAIYVGSKQI 216
QY	215 LAKSWSNDITLLTISFTPLIGHVTGELLALFTHQSQRCRTISLEFGAONIQCITML 274
DB	217 LTTG----LPIFLVLIHLNVLYGTYIGYMLARLLKLRDQKAVSIEVGMONSLAVSLA 271
QY	275 QLSF 278
DB	272 ALHF 275
RESULT 14	
OBV16	
ID	PRELIMINARY; PRT; 318 AA.
AC	OBV16.
DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Sodium/bile acid cotransporter homolog, SBF family.
GN	BME10346.
OS	Brucella melitensis.
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC	Brucellaceae; Brucella.
OX	NCBI_TaxID=29459;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=16M / ATCC 23456 / BIOTYPE 1;
EX	MEDLINE=20020109; PubMed=11756688;
RA	Delvecchio V.G., Kaparatl V., Redkar R.J., Patra G., Mujer C., Los T.,
RA	Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,

THIS PAGE BLANK (USPTO)